

##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
REFERENCE
#authors
#journal
#title
#cross-references MUID:91090841
#accession A36555
#molecule-type mRNA
#residues 1-455 ##label HIM
#cross-references GB:M63121; NID:g339755; PIDN:AAA6754.1; PID:g339756
#accession C36555
#molecule-type protein
#residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;
107-128;162-167,'X',169-201 ##label R12
#note the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor

REFERENCE
#authors
#journal
#title
#cross-references MUID:91017509
#accession A38281
#molecule-type mRNA
#residues 1-455 ##label GRA
#cross-references GB:M37764
#note the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Leu, and GAC for residue 427 as Asn

REFERENCE
#authors
#journal
#title
#cross-references MUID:91006021
#accession S12057
#molecule-type mRNA
#residues 1-455 ##label NOP
#cross-references EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
#note parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were confirmed by protein sequencing

REFERENCE
#authors
#journal
#title
#cross-references MUID:94085779
#accession J70758
#molecule-type DNA
#residues 1-13 ##label KEM
#cross-references MUID:94085779
#note Secckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.

REFERENCE
#authors
#journal
#title
#cross-references MUID:90292116
#accession A60231
#molecule-type protein
#residues 41-43,'X',45-53,'X',55-57 ##label SEL
#note Eur. J. Immunol. (1990) 20:1167-1174
Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.

Best Available Copy

##authors
#journal
#title
#cross-references MUID:91062364
#accession A38258
#molecule-type protein
#residues 41-60 ##label GAT
#experimental-source cancer patient serum

REFERENCE
#authors
#journal
#title
#cross-references MUID:89171156
#accession A60594
#molecule-type protein
#residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
#experimental-source renal failure patient urine

REFERENCE
#authors
#journal
#title
#cross-references MUID:90110215
#accession A35010
#molecule-type protein
#residues 41-45 ##label ENG
#experimental-source normal urine

REFERENCE
#authors
#journal
#title
#cross-references MUID:95128033
#accession JC2404
#molecule-type protein
#residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
##label KAV
#experimental-source urine
#note This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

GENETICS
#gene
#cross-references GDB:125913; OMIM:191190
#map-position 12p13.2-12p13.2
#introns 13/3; 65/1; 108/1; 158/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
KEYWORDS
#domain signal sequence #status predicted #label SIG
#product tumor necrosis factor receptor type 1 #status predicted #label MAT
#domain extracellular #status predicted #label EXT
#product TNF binding protein 1 (tumor necrosis factor-alpha inhibitor) #status experimental #label TBP1
#domain NGF receptor repeat homology #label NG1
#domain NGF receptor repeat homology #label NG2
#domain NGF receptor repeat homology #label NG3
#domain NGF receptor repeat homology #label NG4
#domain transmembrane #status predicted #label MEM
#domain intracellular #status predicted #label INT
#binding-site carboxylate (Asn) (covalent) #status predicted

SUMMARY
#length 455 #molecular-weight 50494 #checksum 153

S. Park and colleagues

6/15/99

End copy

Sleaved Conf A170 v A

Query Match 100.0%; Score 202; DB 1; Length 455;
 Best Local Similarity 96.4%; Pred. No. 6,356-36;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPISGDRKRDSCPOGKYHPQNSI 57
 1 LVPISGDRKRDSCPOGKYHPQNSI 28

RESULT 2
 ENTRY 157826 #type complete
 TITLE tumor necrosis factor receptor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999

ACCESSIONS 157826
 REFERENCE 157826
 #authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
 #journal Mol. Immunol. (1993) 30:165-176
 #title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.

*cross-references MUID:9156721
 #accession 157826
 #status preliminary: translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 1-454 #label RES
 #cross-references GB:M60468; NID:9202100; PIDN:AAA40465.1; PID:9202102

GENETICS
 #gene TNFR-2
 #introns 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
 CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology cytochrome receptor

KEYWORDS
 FEATURE 44-82
 SUMMARY #domain NGF receptor repeat homology #label NGF
 #length 454 #molecular_weight 50030 #checksum 4267

Query Match 83.7%; Score 169; DB 2; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1,196-26;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 30 LVPISGDRKRDSCPOGKYVHSKNSI 57
 1 LVPISGDRKRDSCPOGKYVHSKNSI 28

RESULT 3
 ENTRY 3
 TITLE GOMST1 #type complete
 ALTERNATE_NAMES tumor necrosis factor receptor 1 precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999

ACCESSIONS A38634; B40254; S16677; S19021; I54532
 REFERENCE A38634
 #authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
 #title Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.

*cross-references MUID:91187865
 #accession A38634
 #molecule_type mRNA
 #residues 1-454 #label LEW
 #cross-references GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

REFERENCE A40254
 #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, M.O.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
 #journal Mol. Cell. Biol. (1991) 11:3020-3026
 #title Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.

*cross-references MUID:91246168
 #accession B40254
 #molecule_type mRNA
 #residues 1-454 #label GO2
 #cross-references GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

REFERENCE S16677
 #authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissomergis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
 #journal Eur. J. Immunol. (1991) 21:1649-1656
 #title Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.

*cross-references MUID:91285014
 #accession S16677
 #molecule_type mRNA
 #residues 1-454 #label BAR
 #cross-references EMBL:X59238; NID:953578; PIDN:CAA1922.1; PID:953579

REFERENCE S19021
 #authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
 #journal Immunogenetics (1991) 34:338-340
 #title Molecular cloning and expression of the mouse Tnf receptor type b.

*cross-references MUID:92039815
 #accession S19021
 #molecule_type mRNA
 #residues 1-454 #label ROT
 #cross-references EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:954849

REFERENCE S14532
 #authors Bebo, B.F.
 #journal Immunogenetics (1994) 39:450-451
 #title Nucleotide sequence of the TNF type I receptor from a mouse endothelial cell line.

*cross-references MUID:94245292
 #accession I54532
 #status translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-454 #label RES
 #cross-references GB:J26349; NID:9430732; PIDN:AAA59361.1; PID:9430733

COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoksin).

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS
 FEATURE 1-29
 SUMMARY #domain signal sequence #status predicted #label SIG
 #product tumor necrosis factor receptor type 1 #status predicted #label MAT
 #domain extracellular #status predicted #label EXT
 30-212 #domain NGF receptor repeat homology #label NG1
 44-82 #domain NGF receptor repeat homology #label NG1
 84-126 #domain NGF receptor repeat homology #label NG2
 127-167 #domain NGF receptor repeat homology #label NG3
 168-204 #domain NGF receptor repeat homology #label NG4
 213-235 #domain transmembrane #status predicted #label MEM
 236-454 #domain intracellular #status predicted #label INT
 54,151,202 #binding site carbohydrate (asn) (covalent) #status predicted

Query Match 83.7%; Score 169; DB 1; Length 454;
 Best Local Similarity 78.6%; Pred. No. 1,196-26;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 30 LVPISGDRKRDSCPOGKYVHSKNSI 57
 1 LVPISGDRKRDSCPOGKYVHSKNSI 28

RESULT 4
 ENTRY 4
 TITLE GORTT1 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999

 W P E S E L I
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Apr 18 11:05:55 2000; Maspar time 47.51 Seconds
 Tabular output not generated. 27.800 Million cell updates/sec

Title: >PEP1.PEP
 Description: (1.28) from new.pep
 Perfect Score: 202
 Sequence: 1 lvpnlgtrekrdsvepgqkyhpxnsl 28

Scoring table: PAM 150
 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: P1r62
 1:plrl 2:plr2 3:plr3 4:plr4

Statistics: Mean 29.032; Variance 38.204; scale 0.760

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	202	100.0	455	1	GQHUT1	6.35e-36
2	169	83.7	454	2	tumor necrosis factor	1.19e-26
3	169	83.7	454	1	GOMST1	1.19e-26
4	167	82.7	461	1	GOMST1	4.24e-26
5	155	76.7	461	2	tumor necrosis factor	8.18e-23
6	74	36.6	213	2	hypothetical protein	9.88e-03
7	63	31.2	518	2	hypothetical protein	1.57e+00
8	63	31.2	518	2	hypothetical protein	1.57e+00
9	63	31.2	518	2	hypothetical protein	1.57e+00
10	63	31.2	518	2	hypothetical protein	1.57e+00
11	63	31.2	518	2	hypothetical protein	1.57e+00
12	63	31.2	518	2	hypothetical protein	1.57e+00
13	62	30.7	699	2	DNA-directed RNA poly	2.43e+00
14	62	30.7	699	2	DNA-directed RNA poly	2.43e+00
15	62	30.7	699	2	DNA-directed RNA poly	2.43e+00
16	62	30.7	699	2	DNA-directed RNA poly	2.43e+00
17	61	30.2	451	2	exogenous DNA-binding	3.73e+00
18	61	30.2	451	2	exogenous DNA-binding	3.73e+00
19	61	30.2	451	2	exogenous DNA-binding	3.73e+00
20	61	30.2	451	2	exogenous DNA-binding	3.73e+00
21	60	29.7	363	2	hypothetical protein	3.73e+00
22	60	29.7	363	2	hypothetical protein	3.73e+00
23	60	29.7	363	2	hypothetical protein	3.73e+00

24	60	29.7	1000	2	JF0110	Dis3p protein - human	5.70e+00
25	60	29.7	3034	2	TJ4119	seven pass transmembr	5.70e+00
26	59	28.2	169	2	T04285	hypothetical protein	8.67e+00
27	59	28.2	396	2	I75615	mammary tumor integra	8.67e+00
28	59	29.2	406	2	S42394	G-box-binding protein	8.67e+00
29	59	29.2	636	2	S41067	collagen alpha 1(III)	8.67e+00
30	59	29.2	948	2	A34416	hydroxymethylglutaryl	8.67e+00
31	59	29.2	1464	2	S59856	collagen alpha 1(III)	8.67e+00
32	59	29.2	1466	1	GQHUT1	collagen alpha 1(III)	8.67e+00
33	59	29.2	3433	1	GMWVKV	genome polypeptide	8.67e+00
34	58	28.7	97	2	S62625	hydrophobin HFB1 - fu	1.31e+01
35	58	28.7	155	2	F69190	conserved hypothetical	1.31e+01
36	58	28.7	289	2	B32459	Na+/K+-exchanging ATP	1.31e+01
37	58	28.7	290	2	UC5108	Na+/K+-exchanging ATP	1.31e+01
38	58	28.7	304	2	I50721	synemin - chicken (fr	1.31e+01
39	58	28.7	416	1	KIVKGL	DNA-directed RNA poly	1.31e+01
40	58	28.7	880	1	B33926	DNA-directed RNA poly	1.31e+01
41	58	28.7	1765	2	A31494	DNA-directed RNA poly	1.31e+01
42	58	28.7	1766	2	B31875	DNA-directed RNA poly	1.31e+01
43	58	28.7	1766	2	A31875	DNA-directed RNA poly	1.31e+01
44	58	28.7	3432	1	GMWVJS	genome polypeptide	1.31e+01
45	58	28.7	3432	1	GMWVJE	genome polypeptide	1.31e+01

ALIGNMENTS

RESULT 1
 ENTRY GQHUT1 #type complete
 TITLE tumor necrosis factor receptor 1 precursor - human
 ALTERNATE_NAMES P55 tumor necrosis factor receptor; TNF receptor
 CONTAINS tumor necrosis factor; alpha inhibitor; tumor necrosis factor
 binding protein 1 (TNF blocking factor)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999

ACCESSIONS
 A38208: A34899; A34900; A36555; C36555; A38281; S12057;
 J07058; A60231; A38256; A60594; A35010; J02404

REFERENCE
 #authors Fuchs, P.; Strehl, S.; Dworzak, M.; Hummler, A.; Ambros, P.F.
 #journal Genomics (1992) 13:219-224
 #title Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 localization to chromosome 12p13.
 #cross-references MIM:92250049
 #accession A38208
 ##molecule_type DNA
 ##residues 1-455 #label FUC
 ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:9339748;
 P1DN:AAA61201.1; P1D:9339750

REFERENCE
 #authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
 M.; Tabuchi, H.; Lesslauer, W.
 #journal Cell (1990) 61:351-359
 #title Molecular cloning and expression of the human 55 kd tumor
 necrosis factor receptor.
 #cross-references MIM:90235284
 #accession A34899
 ##molecule_type mRNA
 ##residues 1-455 #label LOE
 ##cross-references GB:M58286; GB:M3480; NID:9339753; P1DN:AAA36753.1;
 P1D:9339754
 ##experimental_source placenta
 ##note part of this sequence, including the amino end of the
 mature protein, confirmed by protein sequencing

REFERENCE
 #authors Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
 Wong, G.H.W.; Galanaga, T.; Granger, G.A.; Lenz, R.; Raab,
 H.; Kohr, W.J.; Goeddel, D.V.
 #journal Cell (1990) 61:361-370
 #title Molecular cloning and expression of a receptor for human
 tumor necrosis factor.
 #cross-references MIM:90235285
 #accession A34900
 ##molecule_type mRNA

Seabuck Comp Alt 70 A

```

Query Match      100.0%; Score 202; DB 1; Length 455;
Best Local Similarity 96.4%; Pred. No. 6.35e-36;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db
30 LYPHGLDRERKDSVCPGKYIHPQXNSI 57
|||||
1 LYPHGLDRERKDSVCPGKYIHPQXNSI 28

RESULT 2
ENTRY      157826 #type complete
TITLE      tumor necrosis factor receptor - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
23-Jul-1999

ACCESSIONS
REFERENCE  157826
#authors   Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
#journal   Mol. Immunol. (1993) 30:165-176
#title     Genomic organization and promoter function of the murine
#cross-references MUID:93156721
#accession 157826
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  1-454 #label RES
#cross-references GB:M76656; NID:g202100; PID:AAA0465.1; PID:g202102

GENETICS
#gene       TNFR-2
#introns    13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
#keywords   cytokine receptor

FEATURES
FEATURE     44-82
SUMMARY     #domain NGF receptor repeat homology #label NGF
#length 454 #molecular-weight 50030 #checksum 4267

Query Match      83.7%; Score 169; DB 2; Length 454;
Best Local Similarity 78.6%; Pred. No. 1.19e-26;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db
30 LYPGLDRERKDSICPGKTVHSKNSI 57
|||||
1 LYPHGLDRERKDSVCPGKYIHPQXNSI 28

RESULT 3
ENTRY      GONST1 #type complete
TITLE      tumor necrosis factor receptor 1 precursor - mouse
ALTERNATE_NAMES #formal_name Mus musculus #common_name house mouse
ORGANISM       30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE           22-Jun-1999
ACCESSIONS     A38634; B40254; S16677; S19021; I54532
REFERENCE      A38634
#authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
#journal       G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.;
#title         Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#cross-references MUID:91187885
#accession     A38634
#molecule_type mRNA
#residues      1-454 #label LEW
#cross-references GB:M00468; NID:g199825; PID:AAA39751.1; PID:g199826

AUTHORS
#journal       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
#journal       C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.;
#journal       Mol. Cell. Biol. (1991) 11:3020-3026
#journal       Molecular cloning and expression of the type 1 and type 2
#journal       murine receptors for tumor necrosis factor.

```

```

#cross-references MUID:91246168
#accession     B40254
#molecule_type mRNA
#residues      1-454 #label GO2
#cross-references GB:M00468; NID:g199825; PID:AAA39751.1; PID:g199826

REFERENCE      S16677
#authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissmerghis,
#journal       A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
#title         Eur. J. Immunol. (1991) 21:1649-1656
#cross-references MUID:91285014
#accession     S16677
#molecule_type mRNA
#residues      1-454 #label BAR
#cross-references EMBL:X59238; NID:g53578; PID:CAA41922.1; PID:g53579

REFERENCE      S19021
#authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
#journal       Immunogenetics (1991) 34:338-340
#title         Molecular cloning and expression of the mouse Tnf receptor
#cross-references MUID:92039815
#accession     S19021
#molecule_type mRNA
#residues      1-454 #label ROT
#cross-references EMBL:X57796; NID:g54848; PID:CAA40936.1; PID:g54849

REFERENCE      I54532
#authors       Bebo, B.F.
#journal       Nucleic Acids Res. (1994) 22:450-451
#title         Nucleotide sequence of the TNF type I receptor from a mouse
#cross-references MUID:94245292
#accession     I54532
#status        translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      1-454 #label RES
#cross-references GB:I26349; NID:g430732; PID:AAA59361.1; PID:g430733

COMMENT        This protein is one of two distantly related receptors for both
#cross-references MUID:94245292
#accession     I54532
#status        translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      1-454 #label RES
#cross-references GB:I26349; NID:g430732; PID:AAA59361.1; PID:g430733

CLASSIFICATION TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
#superfamily tumor necrosis factor receptor type 1; NGF
#keywords       duplication; glycoprotein; receptor; transmembrane protein
FEATURE         1-29
SUMMARY         #domain signal, sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 1 #status
#predicted #label MAT\
#domain extracellular #status predicted #label EXT\
30-212          #domain NGF receptor repeat homology #label NG1\
44-82           #domain NGF receptor repeat homology #label NG2\
84-126         #domain NGF receptor repeat homology #label NG3\
127-167        #domain NGF receptor repeat homology #label NG4\
168-204        #domain NGF receptor repeat homology #label NG5\
213-235        #domain transmembrane #status predicted #label MEM\
236-454        #domain intracellular #status predicted #label INT\
54,151,202     #binding site carbohydrate (Asn) (covalent) #status
                predicted

Query Match      83.7%; Score 169; DB 1; Length 454;
Best Local Similarity 78.6%; Pred. No. 1.19e-26;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db
30 LYPGLDRERKDSICPGKTVHSKNSI 57
|||||
1 LYPHGLDRERKDSVCPGKYIHPQXNSI 28

RESULT 4
ENTRY      GORT1 #type complete
TITLE      tumor necrosis factor binding protein 1 (TNF blocking factor)
ALTERNATE_NAMES #formal_name Rattus norvegicus #common_name Norway rat
ORGANISM       30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
DATE           22-Jun-1999

```

```

ACCESSIONS      B36555
REFERENCE        A36555
#authors        Himmler, A.; Maurer-Foy, I.; Krenke, M.; Scheurich, P.;
#journal        Pflüger, K.; Lant, M.; Olsson, I.; Hauptmann, R.;
#title          DNA Cell Biol. (1990) 9:705-715
#cross-references MUID:91090841
#accession      B36555
#molecule_type mRNA
#residues       1-461 #label HIM
#cross-references GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
COMMENT          This protein is one of two known receptors for both TNF-alpha
                  (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS         duplication; glycoprotein; receptor; transmembrane protein
FEATURE         1-29      #domain signal sequence #status predicted #label sig\
                  30-461  #product tumor necrosis factor receptor type 1 #status
                  30-201  #domain extracellular #status predicted #label ext\
                  44-82   #product tumor necrosis factor binding protein #status
                  84-126  #predicted #label TBP\
                  127-167 #domain NGF receptor repeat homology #label NG1\
                  168-204 #domain NGF receptor repeat homology #label NG2\
                  212-234 #domain NGF receptor repeat homology #label NG3\
                  235-461 #domain NGF receptor repeat homology #label NG4\
                  54,151,201 #domain transmembrane #status predicted #label MEM\
                  #domain intracellular #status predicted #label INT\
                  #binding_site carbohydrate (Asn) (covalent) #status
                  predicted
SUMMARY          #length 461 #molecular-weight 50969 #checksum 1617
Query Match      82.7%; Score 167; DB 1; Length 461;
Best Local Similarity 78.6%; Pred. No. 4; 24e-26;
Matches 22; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db               30 LVPISLGRKRDNLCPGKRYAHPKNNST 57
               ||| |||||:::||||| || |||
Oy               1 lvpghgdrkrdsvcpqgkyhnpqnsi 28

RESULT          5
ENTRY           JC4302      #type complete
TITLE           tumor necrosis factor receptor p55 precursor - pig
ORGANISM        #formal_name Sus scrofa domestica #common_name domestic pig
DATE            29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                23-Jul-1999
ACCESSIONS      JC4302; PC4093
REFERENCE        JC4302
#authors        Suter, B.; Pauli, U.
#journal        Gene (1995) 163:263-266
#title          Cloning of the cDNA encoding the porcine p55 tumor necrosis
                  factor receptor.
#cross-references MUID:96011645
#accession      JC4302
#molecule_type mRNA
#residues       1-461 #label SUT
#cross-references GB:U19994; NID:g1141752; PIDN:AAC48499.1;
                  PID:g1141753
#accession      PC4093
#molecule_type protein
#residues       1-7 #label SUT
#experimental_source kidney cell line 15
GENETICS         #superfamily tumor necrosis factor receptor type 1; NGF
                  receptor repeat homology
KEYWORDS         glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE

```

```

1-29      #domain signal sequence #status predicted #label SIG\
30-461    #product tumor necrosis factor receptor p55 #status
          predicted #label MAF\
44-194     #domain extracellular cysteine rich #status predicted
          #label EXT\
44-82      #domain NGF receptor repeat homology #label NG1\
84-116     #domain NGF receptor repeat homology #label NGF\
211-231    #domain transmembrane #status predicted #label TM\
361-447     #domain signal transduction #status predicted #label
          S/T\
54,145,151 #binding_site carbohydrate (Asn) (covalent) #status
           predicted
SUMMARY    #length 461 #molecular-weight 50696 #checksum 8079

Query Match       76.7%; Score 155; DB 2; Length 461;
Best Local Similarity 75.0%; Pred. No. 8.18e-23;
Matches 21; Conservative 2; Misses 5; Indels 0; Gaps 0;

Db            30 LYLHPGDRKRRESLCPQGYKSHPNQNSI 57
              ||| | | | | | | | | | | | | | | |
              1 lvphtgdrkrdsvcpqgykshpnqxnsi 28

RESULT      6
ENTRY
TITLE       C69980 #type complete
ORGANISM    hypothetical protein yrrT - Bacillus subtilis
DATE        05-Dec-1997 #sequence_revision 05-Dec-1997 #text-change
                24-Sep-1998
ACCESSIONS  C69980
REFERENCE   A69580
#AUTHORS    Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
              Allion, G.; Azevedo, V.; Besterio, M.G.; Bessières, P.;
              Bolotin, A.; Borcherdt, S.; Boris, R.; Bourcier, L.; Brans,
              A.; Braun, M.; Brignell, S.C.; Bron, S.; Broillet, S.;
              Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
              Choi, S.K.; Codani, J.J.; Conerton, I.F.; Cummings, N.J.;
              Daniel, K.A.; Denizot, F.; Devlane, K.M.; Duesterhoelt, A.;
              Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.;
              Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
              M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Galleron, N.; Glum,
              S.Y.; Glaeser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
              Gulseppel, G.; Guy, B.-J.; Haga, A.; Halech, J.; Harwood,
              C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
              Hullio, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karimata, D.;
              Kashara, Y.; Kleier-Blanchard, M.; Klein, C.; Kobayashi,
              Y.; Koetter, P.; Kontagstein, G.; Krogh, S.; Kumano, M.;
              Kurita, K.; Lapidus, A.; Lardinols, S.; Lauber, J.;
              Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
              Mauviel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
              M.; Moestil, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
              M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro,
              V.; Poll, T.M.; Portetalle, D.; Porwollik, S.; Prescott,
              A.M.; Presecan, E.; Pujić, P.; Punelle, B.; Rapoport, G.;
              Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
              Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
              Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
              Sekowska, A.; Seror, S.J.; Serrou, P.; Shin, B.S.; Soldo,
              B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
              Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.;
              Teysstra, P.; Toignon, A.; Tosato, V.; Uchiyama, S.;
              Vandenbulc, M.; Vannier, F.; Vassartelli, A.; Viari, A.;
              Wandut, R.; Wedler, E.; Weller, H.; Weltensberger, T.;
              Winers, P.; Wißat, A.; Yamamoto, H.; Yamane, K.; Yasunoto,
              Y.; Yata, K.; Yoshida, K.; Yoshioka, H.F.; Zumbach, E.;
              Yoshikawa, H.; Danchin, A.
              Nature (1997) 390:249-256
              The complete genome sequence of the Gram-positive bacterium
              Bacillus subtilis.
              PMID:98044033
C69980
#cross-references WCID:98044033
#accession
#status
#title
#journal
#file
#preliminary: nucleic acid sequence not shown;
translation not shown

```

```

##molecule_type DNA
##residues 1-213 ##label KUN
##cross-references GB:Z99117; GB:A009126; NID:g2634966; PID:e1183958;
##experimental_source strain 168
GENETICS
#gene
#introns
#exons
SUMMARY
#length 213 #molecular-weight 24196 #checksum 2669

Query Match
Best Local Similarity 40.0%; Score 74; DB 2; Length 213;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Db 119 HLTDEKRAIKYGTIHLHDKY 143
119 HLTDEKRAIKYGTIHLHDKY 143
4 hlgdrekrdsvcpqgkyihpdxnsi 28

RESULT 7
ENTRY H70388 #type complete
TITLE selenophosphate synthase - Aquifex aeolicus
ALTERNATE_NAMES #formal_name Aquifex aeolicus
ORGANISM 08-May-1998 #sequence_revision 08-May-1998 #text_change
DATE 08-May-1998
ACCESSIONS H70388
REFERENCE A70300
AUTHORS Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
#accession Aquifex aeolicus.
#cross-references M01D:98196666
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-311 ##label AQF
##cross-references GB:A000719; NID:g2983517; PID:g2983519; GB:A000657
##experimental_source strain VFS
GENETICS
#gene
#introns
#exons
SUMMARY
#length 311 #molecular-weight 34231 #checksum 842

Query Match
Best Local Similarity 66.7%; Score 63; DB 2; Length 311;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 122 GICPEGRYI 130
122 GICPEGRYI 130
13 svcpqgkyi 21

RESULT 8
ENTRY T07942 #type complete
TITLE probable squalene monooxygenase (EC 1.14.99.7) Sqp1 - rape
ALTERNATE_NAMES #formal_name Brassica napus #common_name rape
ORGANISM 21-May-1999 #sequence_revision 21-May-1999 #text_change
DATE 11-Jun-1999
ACCESSIONS T07942
REFERENCE Z16234
AUTHORS Schaefer, U.A.; Reed, D.W.; Hunter, D.G.; Yao, K.; Weninger,
A.M.; Tsang, E.W.T.; Reaney, M.J.T.; Mackenzie, S.L.;
Covello, P.S.
#journal Plant Mol. Biol. (1999) 39:721-728
#title An example of intron junctional sliding in the gene families
#accession encoding squalene monooxygenase homologues in Arabidopsis
#status thaliana and Brassica napus.
#molecule_type mRNA
#accession T07942
#cross-references EMBL:Z16234; NID:g60497; PID:CAA78263.1; PID:g60498
#superfamily translated from GB/EMBL/DBJ
#length 563 #molecular-weight 62883 #checksum 792

```

```

##residues 1-506 ##label SCH
##cross-references EMBL:A005931; NID:e1291750; PID:e1291751
##experimental_source cv. Westar; developmental stage:
greenling-etiolated; tissue type: shoots
GENETICS
#gene
#introns
#exons
SUMMARY
#length 506 #molecular-weight 55571 #checksum 5540

Query Match
Best Local Similarity 31.2%; Score 63; DB 2; Length 506;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Db 74 HYERDMREPRVPMGEFMP 93
74 HYERDMREPRVPMGEFMP 93
4 hlgdrekrdsvcpqgkyihp 23

RESULT 9
ENTRY T07940 #type complete
TITLE probable squalene monooxygenase (EC 1.14.99.7) Sqp2 - rape
ALTERNATE_NAMES #formal_name Brassica napus #common_name rape
ORGANISM 21-May-1999 #sequence_revision 21-May-1999 #text_change
DATE 11-Jun-1999
ACCESSIONS T07940
REFERENCE Z16234
AUTHORS Schaefer, U.A.; Reed, D.W.; Hunter, D.G.; Yao, K.; Weninger,
A.M.; Tsang, E.W.T.; Reaney, M.J.T.; Mackenzie, S.L.;
Covello, P.S.
#journal Plant Mol. Biol. (1999) 39:721-728
#title An example of intron junctional sliding in the gene families
#accession encoding squalene monooxygenase homologues in Arabidopsis
#status thaliana and Brassica napus.
#molecule_type mRNA
#residues 1-518 ##label SCH
##cross-references EMBL:A005928; NID:e1291748; PID:e1291749
##experimental_source cv. Westar; developmental stage:
greenling-etiolated; tissue type: shoots
GENETICS
#gene
#introns
#exons
SUMMARY
#length 518 #molecular-weight 57399 #checksum 7018

Query Match
Best Local Similarity 30.0%; Score 63; DB 2; Length 518;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Db 75 HYERDMREPRVPMGEFMP 94
75 HYERDMREPRVPMGEFMP 94
4 hlgdrekrdsvcpqgkyihp 23

RESULT 10
ENTRY S22083 #type complete
TITLE hemagglutinin - Influenza A virus
ALTERNATE_NAMES #formal_name Influenza A virus
ORGANISM 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
DATE 20-Sep-1999
ACCESSIONS S22083
REFERENCE S22083
AUTHORS Garten, W.D.
#journal submitted to the EMBL Data Library, May 1992
#accession S22083
#status preliminary
#molecule_type DNA
#residues 1-563 ##label GAR
#cross-references EMBL:S22083; NID:g60497; PID:CAA78263.1; PID:g60498
#superfamily translated from GB/EMBL/DBJ
#length 563 #molecular-weight 62883 #checksum 792

```

accession	E1330
#status	preliminary; nucleic acid sequence not shown; translation not shown

##molecule_type DNA
 ##residues 1-916 ##label COL
 ##cross-references GB:AE001217; GB:AE000520; NID:G3322656;
 PTDN:ACG5365.1; PTD:G3322659
 ##experimental_source strain Nichols

GENETICS

#gene TP0379

CLASSIFICATION

#superfamily preprotein translocase secA; DEAD/H box helicase
 homology
 ATP; P-loop

KEYWORDS

103-599 #domain DEAD/H box helicase homology #label DEAD\
 103-110 #region nucleotide-binding motif A (P-loop)\
 206-211 #region nucleotide-binding motif B\
 210-213 #region DEAD/H motif #status atypical
 #length 916 #molecular-weight 103779 #checksum 4056

SUMMARY

Query Match 30.7%; Score 62; DB 2; Length 916;
 Best Local Similarity 25.9%; Pred. No. 2.43e+00;
 Matches 7; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 433 VTISEEKKWSAICDEIKKAHTKQPV 459

QY 2 vphlgdrekrdsvcpqgkyihpqnsl 28

RESULT 15

ENTRY 15 S63986 #type fragment
 TITLE collagen alpha 5 chain - sea urchin (Strongylocentrotus

ORGANISM

purpuratus) (fragment)
 #formal_name Strongylocentrotus purpuratus #common_name
 purple urchin
 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change
 25-Apr-1997

DATE

ACCESSIONS S63986; S64638
 REFERENCE S63985

AUTHORS

Exposito, J. Y.; Boure, N.; Delage, G.; Garrone, R.
 Eur. J. Biochem. (1995) 234:55-65

JOURNAL

Characterization of two genes coding for a similar
 four-cysteine motif of the amino-terminal propeptide of a
 sea urchin fibillar collagen.

#cross-references MVID:96096722

#accession S63986

##status nucleic acid sequence not shown

##molecule_type DNA

##residues 1-1376 #label EXP

##cross-references EMBL:X83804

REFERENCE S64637

#authors Exposito, J. Y.
 #submission submitted to the EMBL Data Library, July 1995

#accession S64638

#molecule_type DNA

1-658, 'G', 660-870, 'G', 872-901, 'H', 903-1185, 'T',
 1187-1214, 'Y', 1216-1376 #label EXM

##cross-references EMBL:X83804

GENETICS

#gene COLP5alpha

#introns 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1;
 1093/1; 1236/1

CLASSIFICATION

#superfamily von Willebrand factor type C repeat homology
 extracellular matrix

KEYWORDS

FEATURE

15-73

#domain von Willebrand factor type C repeat homology
 #label VMC

SUMMARY

#length 1376 #checksum 7553

Query Match

Best Local Similarity 30.7%; Score 62; DB 2; Length 1376;
 Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Db 890 FVPLVTNFDMDLKCPOVKTCNEVN 915

QY 1 lvphlgdrekrdsvcpqgkyihpqn 26

 M P E R S E R E H
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit,
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Apr 18 11:07:05 2000; Maspar time 27.80 Seconds
 Tabular output not generated. 30.077 Million cell updates/sec

Title: >PEP1.PEP
 Description: (1-28) from new.pep
 Perfect Score: 202
 Sequence: 1 lvphlgdrekidsvcpgkyihpqxst 28

Scoring table:
 PAM 150
 Gap 15

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot8
 1:swissprot

Statistics: Mean 29.784; Variance 34.076; scale 0.874

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	202	100.0	455	1 TNRI_HUMAN	TUMOR NECROSIS FACTOR	2.05e-41
2	169	83.7	454	1 TNRI_MOUSE	TUMOR NECROSIS FACTOR	8.20e-31
3	167	82.7	461	1 TNRI_RAT	TUMOR NECROSIS FACTOR	3.50e-30
4	155	76.7	461	1 TNRI_PIG	TUMOR NECROSIS FACTOR	1.98e-26
5	63	31.2	336	1 SEID_AQUAE	SELENIDE WATER DIKINAS	3.94e-01
6	63	31.2	1442	1 CPSE_HUMAN	CLEAVAGE AND POLYADENT	3.94e-01
7	63	31.2	1444	1 CPSE_BOVIN	CLEAVAGE AND POLYADENT	3.94e-01
8	62	30.7	264	1 RPOD_SOLAC	DNA-DIRECTED RNA POLYM	6.40e-01
9	62	30.7	916	1 SECA_TREPA	PREPROTEIN TRANSLOCASE	6.40e-01
10	61	30.2	98	1 CMG3_BACSU	COMG OPERON PROTEIN 3	1.03e+00
11	60	29.7	148	1 NOL1_RHIFR	MODULATION PROTEIN NOL	1.66e+00
12	59	29.2	140	1 YB18_SCHPO	HYPOTHETICAL 16.2 KD P	2.65e+00
13	59	29.2	445	1 INT6_MOUSE	VIRAL INTEGRATION SITE	2.65e+00
14	59	29.2	473	1 PPS1_HUMAN	PHOSPHATIDYL SERINE SYN	2.65e+00
15	59	29.2	568	1 G6P1_CLAMI	GLUCOSE-6-PHOSPHATE IS	2.65e+00
16	59	29.2	636	1 CA13_RAT	COLLAGEN ALPHA 1(III)	2.65e+00
17	59	29.2	948	1 HMDH_SCHMA	3-HYDROXY-3-METHYLGIDT	2.65e+00
18	59	29.2	1464	1 CA13_MOUSE	COLLAGEN ALPHA 1(III)	2.65e+00
19	59	29.2	1466	1 CA13_HUMAN	COLLAGEN ALPHA 1(III)	2.65e+00
20	59	29.2	3433	1 POLG_KUNJM	GENOME POLYPROTEIN (CO	2.65e+00
21	58	28.7	97	1 HYP1_TRIRE	HYDROPHOBIN I PRECURSOR	4.20e+00
22	58	28.7	290	1 ATNC_BOVIN	SODIUM/POTASSIUM-TRANS	4.20e+00
23	58	28.7	290	1 ATNC_HUMAN	SODIUM/POTASSIUM-TRANS	4.20e+00

24	58	28.7	290	1 ATNC_MOUSE	SODIUM/POTASSIUM-TRANS	4.20e+00
25	58	28.7	290	1 ATNC_RAT	SODIUM/POTASSIUM-TRANS	4.20e+00
26	58	28.7	416	1 PKR_KLULA	PHOSPHOGLYCERATE KINAS	4.20e+00
27	58	28.7	569	1 G6P2_CLACO	GLUCOSE-6-PHOSPHATE IS	4.20e+00
28	58	28.7	570	1 G6P1_CLARO	GLUCOSE-6-PHOSPHATE IS	4.20e+00
29	58	28.7	683	1 PLO1_SCHPO	SERINE/THREONINE-PROTE	4.20e+00
30	58	28.7	880	1 RPA1_SULAC	DNA-DIRECTED RNA POLYM	4.20e+00
31	58	28.7	1079	1 IFP2_SCHPO	PROBABLE TRANSLATION I	4.20e+00
32	58	28.7	1766	1 RPA2_TRYBB	DNA-DIRECTED RNA POLYM	4.20e+00
33	58	28.7	1766	1 RPA1_TRYBB	DNA-DIRECTED RNA POLYM	4.20e+00
34	58	28.7	3432	1 POLG_JAEVJ	GENOME POLYPROTEIN (CO	4.20e+00
35	58	28.7	3432	1 POLG_JAEVJ	GENOME POLYPROTEIN (CO	4.20e+00
36	58	28.7	3432	1 POLG_JAEVJ	GENOME POLYPROTEIN (CO	4.20e+00
37	57	28.2	377	1 YTXN_BACSU	HYPOTHETICAL 42.9 KD P	6.61e+00
38	57	28.2	469	1 DPD2_BOVIN	DNA POLYMERASE DELTA S	6.61e+00
39	57	28.2	476	1 U136_HCMVA	HYPOTHETICAL PROTEIN U	6.61e+00
40	57	28.2	698	1 TRPE_RAT	SEROTRANSFERIN PRECUR	6.61e+00
41	57	28.2	827	1 RAPI_YEAST	DNA-BINDING PROTEIN RA	6.61e+00
42	57	28.2	859	1 PMS2_MOUSE	PMS1 PROTEIN HOMOLOG 2	6.61e+00
43	57	28.2	862	1 PMS2_HUMAN	PMS1 PROTEIN HOMOLOG 2	6.61e+00
44	57	28.2	1210	1 EGFR_HUMAN	EPIDERMAL GROWTH FACTO	6.61e+00
45	56	27.7	568	1 G6P1_CLAYA	GLUCOSE-6-PHOSPHATE IS	1.03e+01

ALIGNMENTS

RESULT ID	1	TNRI_HUMAN	STANDARD:	PRF:	455 AA.
AC	P19438;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR				
DE	BINDING PROTEIN 1) (TBP1) (P60) (TNF-R1) (P95) (CD120A).				
GN	TNFRSF1A OR TNFR1 OR TNFR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE-PLACENTA;				
RC	MEDLINE: 90235285.				
RX	SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,				
RA	GETNAGA T., GRANGER G.A., LEMTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.,				
RT	"Molecular cloning and expression of a receptor for human tumor				
RT	necrosis factor."				
RL	Cell 61:361-370(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 90235284.				
RX	LOEFSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,				
RA	TABUCHI H., LESSLAUER W.,				
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis				
RT	factor receptor."				
RL	Cell 61:351-359(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 91090841.				
RX	HIMMER A., MARRER-FOGY I., KROENKE M., SCHURICH P., PRITZENWATER K.,				
RA	LANZ M., OLSSON I., HADPTMAN R., STATOWA C., ADOLF G.R.,				
RT	"Molecular cloning and expression of human and rat tumor necrosis				
RT	factor receptor chain (p60) and its soluble derivative, tumor				
RT	necrosis factor-binding protein."				

RL DNA Cell Biol. 9:705-715(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91017509.
 RA GRAY P.W., BARRETT K., CHANTREY D., TURNER M., FELDMAN M.;
 RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
 expression of recombinant soluble TNF-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92250049.
 RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMEROS P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 localization to chromosome 12p13.";
 RL Genomics 13:219-224(1992).
 RN [7]
 RP SEQUENCE OF 41-45.
 RX MEDLINE: 90110215.
 RA ENGELMANN H., NOVICK D., WALLACH D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 urine. Evidence for immunological cross-reactivity with cell surface
 tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
 RX MEDLINE: 93258809.
 RA BANNER D.W., D'ARCY A., JAMES W., GENTZ R., SCHOENFELD H.-J.;
 RT BROGER C., LOESCHER H., LESSLAUER W.;
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 beta complex: implications for TNF receptor activation.";
 RL Cell 73:431-445(1993).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE: 97094982.
 RA NAISWITZ J.H., DEVINE T.O., KHONO H., SPRANG S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis
 factor receptor.";
 RL Structure 4:1251-1262(1996).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
 NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
 OF THE ACID SPHINGOMYELINASE.
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120a entry;
 WWW-http://www.ncbi.nlm.nih.gov/prov/ncbi/cd120a.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X55313; CAA39021.1;
 CC EMBL: M33294; AAA03210.1; -
 CC DR

DR EMBL: M58286; AAA36753.1; -
 DR EMBL: M63121; AAA36754.1; -
 DR EMBL: M75866; AAA61201.1; -
 DR EMBL: M75864; AAA61201.1; JOINED.
 DR EMBL: M75865; AAA61201.1; JOINED.
 DR EMBL: M60275; AAA36756.1; -
 DR EMBL: A21522; CAA01558.1; -
 DR PIR: A34899; G0H071.
 DR PIR: A35010; A35010.
 DR PIR: S12057; S12057.
 DR PIR: A38208; A38208.
 DR PDB: ITNR; 3I-JUL-94.
 DR PDB: INCF; 07-DEC-95.
 DR PDB: IEXT; 11-JAN-97.
 DR MIM: 191190; -
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PFAM: PF00531; death; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
 KW 3d-structure.
 FT STGNAL 1 21
 FT CHAIN 22 455
 FT CHAIN 41 291
 FT DOMAIN 22 211
 FT TRANSMEM 212 234
 FT DOMAIN 235 455
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 338 348
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 FT CARBOHYD 412 412
 FT CONFLICT 443 446
 FT CONFLICT 455 AA; 50494 MM; CE0EA065 CXC32;
 SQ SEQUENCE
 Query Match 100.0%; Score 202; DB 1; Length 455;
 Best Local Similarity 96.4%; Pred. No. 2.05e-41;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 30 LYPHLDGDRKRDVSCPOGKTIHPONNSI 57
 1 LYPHLDGDRKRDVSCPOGKTIHPONNSI 28
 RESULT 2
 ID TNFR1_MOUSE STANDARD; PRT; 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91187885.
 RA LEMIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GOEDDEL D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91246168.
 RA GOODWIN R.G., ANDERSON D., JERRY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor."
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91285014.
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
 RA GRAY P.W., FELDMAN M., FOXWELL B.M.J.,
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor."
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-SPLEEN;
 RX MEDLINE; 92039815.
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.,
 RT "Molecular cloning and expression of the mouse Tnf receptor type b."
 RL Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94245232.
 RA BEBO B.F., LINTHICUM D.S.,
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line."
 RL Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93156721.
 RA ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.,
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene."
 RL Mol. Immunol. 30:165-175(1993).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use. By non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; M60468; AAA39751.1; -

DR EMBL; M59377; AAA40464.1; -
 DR EMBL; X59238; CAA41922.1; -
 DR EMBL; X57796; CAA40936.1; -
 DR EMBL; L26349; AAA59361.1; -
 DR EMBL; M76656; AAA40465.1; -
 DR EMBL; M88067; AAA40465.1; JOINED.
 DR EMBL; M76655; AAA40465.1; JOINED.
 DR PIR; A38634; GOMSTL.
 DR PIR; S16677; S16677.
 DR PIR; S19021; S19021.
 DR HSSP; P19438; IEXT.
 DR MGI; MGI:1314884; TNFRSF1A.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR Pfam; PF00020; TNFR_C6; 4.
 DR Pfam; PF00531; death; 1.
 KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT DOMAIN 22 212
 FT TRANSMEM 213 235
 FT DOMAIN 236 454
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 339 349
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 202 202
 FT CONFLICT 394 394
 SQ SEQUENCE 454 AA; 50129 MW; 486EC09 CRC32;
 Query Match 83.7%; Score 169; DB 1; Length 454;
 Best Local Similarity 78.6%; Pred. No. 8, 20e-31;
 Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DB 30 LVPSTGDRKRDLSLCPQKTVHSSKNNST 57
 QY 1 LYPHSGDREKRSVCPGKYHPGXNSI 28
 ID 3
 ID TNFR1_RAT STANDARD; PRT; 461 AA.
 AC P22934;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91090841.
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
 RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;

FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 190 BY SIMILARITY.
 FT DISULFID 185 194 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 145 145 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 SQ SEQUENCE 461 AA; 50696 MW; 8E2C350A CRC32;
 Query Match 76.7%; Score 155; DB 1; Length 461;
 Best Local Similarity 75.0%; Pred. No. 1.98e-26;
 Matches 21; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Db 30 LVLHPGDKREKESICPGKYSHPONRSI 57
 1 LVPHlgdrekrdsvcpqgkylhpqxnsl 28
 RESULT 5
 ID SELD_AQUAE STANDARD; PRT; 336 AA.
 AC 067139;
 DT 15-DEC-1999 (Rel. 39, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DE 15-DEC-1999 (Rel. 39, Last annotation update)
 DE SELENIIDE, WATER DIKINASE (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE)
 GN SELD OR AQ_1030.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-VF5;
 RX MEDLINE; 98196666.
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBEK R., SNEAD M.A., KELLER M., AUCAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RA BAIROCH A.;
 RL Unpublished observations (JUL-1999).
 CC -1- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIIDE AND ATP
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + SELENIIDE + H(2)O = AMP + SELENOPHOSPHATE
 CC + PHOSPHATE.
 CC -1- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).
 CC CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A UGA STOP CODON HAD TO
 CC BE SKIPPED IN POSITION 13 TO PRODUCE THIS ORF. WE (REF.2) BELIEVE
 CC THAT THIS RESIDUE IS MOST PROBABLY AN ACTIVE-SITE SELENOCYSTEINE.
 CC -1- SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
 CC CLASS 1 SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AEO00719; AAC07095.1; ALT_FRAME.
 DR TRANSFERASE; Selenium; Magnesium; ATP-binding; Selenocysteine.
 KM ACT_SITE 13 13 POTENTIAL.
 FT SE_SITE 13 13 POTENTIAL.
 FT SITE 16 16 IMPORTANT FOR CATALYTIC ACTIVITY (BY
 FT SIMILARITY).
 FT NP_BIND 222 228 ATP (POTENTIAL).

SQ SEQUENCE 336 AA; 36809 MW; 297029FE CRC32;
 Query Match 31.2%; Score 63; DB 1; Length 336;
 Best Local Similarity 66.7%; Pred. No. 3.94e-01;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Db 147 GICEPGKXYI 155
 13 svcpqgkyl 21
 RESULT 6
 ID CP5A_HUMAN STANDARD; PRT; 1442 AA.
 AC Q10570;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CP5F
 DE 160 KD SUBUNIT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96067159.
 RA MURPHY K.G., MANLEY J.L.;
 RT "The 160-kD subunit of human cleavage-polyadenylation specificity
 RT factor coordinates pre-mRNA 3'-end formation.";
 RL Genes Dev. 9:2672-2683(1995).
 CC -1- FUNCTION: CP5F PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION.
 CC RECOGNIZING THE AAUAA SIGNAL, SEQUENCE AND INTERACTING WITH
 CC POLY(A) POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
 CC STEP OF THE POLYADENYLATION REACTION.
 CC -1- SUBUNIT: CP5F IS A HETEROTETRAMER COMPOSED OF FOUR DISTINCT
 CC SUBUNITS 160, 100, 70 AND 30 KD.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U37012; AAC50293.1;
 DR NUCLEAR protein; RNA-binding. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 KM DOMAIN 893 908
 FT SEQUENCE 1442 AA; 160822 MW; 8296E75B CRC32;
 SQ SEQUENCE 1442 AA; 160822 MW; 8296E75B CRC32;
 Query Match 31.2%; Score 63; DB 1; Length 1442;
 Best Local Similarity 28.6%; Pred. No. 3.94e-01;
 Matches 8; Conservative 11; Mismatches 8; Indels 1; Gaps 1;
 Db 1047 IPMTGEEKETTERIENDERYTHPOQEA 1074
 2 vphlgdrekrdsvcpqgkylhpqxnsl 28
 RESULT 7
 ID CP5A_BOVIN STANDARD; PRT; 1444 AA.
 AC Q10569;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CP5F
 DE 160 KD SUBUNIT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.

```

RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-THYMUS;
RX MEDLINE: 9538027.
RA JENNY A., KELLER W.;
RT "Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage
RL and polyadenylation specificity factor".
RN Nucleic Acids Res. 23:2629-2635(1995).
[2]
RX CHARACTERIZATION.
RX MEDLINE: 92097544.
RA KELLER W., BIENROTH S., LANG K.M., CRISTOFORI G.;
RT "Cleavage and polyadenylation factor CPF specifically interacts with
RL the pre-mRNA 3' processing signal AAAAA."
RX EMBL J. 10:4241-4249(1991).
CC -1- FUNCTION: CPSE PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION,
CC RECOGNIZING THE AAAAA SIGNAL SEQUENCE AND INTERACTING WITH
CC POLY(A) POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
CC POLY(A) ADDITION. THIS SUBUNIT IS INVOLVED IN THE RNA RECOGNITION
CC STEP OF THE POLYADENYLATION REACTION.
CC -1- SUBUNIT: CPSE IS A HETEROTETRAMER COMPOSED OF FOUR DISTINCT
CC SUBUNITS 160, 100, 70 AND 30 KD.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
CC -1- PFM: THE N-TERMINUS IS BLOCKED.
CC -----
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X83097; CAA58152.1;
RM NUCLEAR protein; RNA-binding.
RM NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
RM DOMAIN.
RM 894 909
RM SEQUENCE 1444 AA; 161214 MW; AC11D659 CRC32;
SQ
Query Match 31.2%; Score 63; DB 1; Length 1444;
Best Local Similarity 28.6%; Pred. No. 3.94e-01;
Matches 8; Conservative 11; Mismatches 8; Indels 1; Gaps 1;
Db 1048 VERMTEGEEKFEETDEREYVHPQDAF 1075
Oy 2 vphlgdrektr-davcpqgyihpqnmsl 28
RESULT 8
ID RPOD_SULAC STANDARD; PRT; 264 AA.
AC P39471;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE SUBUNIT D (Ec 2.7.7.6).
GN RPOD.
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DSM 639;
RX MEDLINE: 95320156.
RA LANGER D., HAIN J., THURIAUX P., ZILLIG W.;
RT "Transcription in archaea: similarity to that in eucarya."
RL Proc. Natl. Acad. Sci. U.S.A. 92:5768-5772(1995).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
CC RNA(N).
CC -1- SUBUNIT: THE S ACIDOCALDIARIUS RNAP IS COMPOSED OF 13 SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE RPB3/RPC5 RNA POLYMERASE SUBUNIT
CC FAMILY.
CC -----

```

```

CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X80194; CAA56480.1;
RM PIR: S47023; S47023.
RM PROSITE: PS00446; RNA_POL.D 30KD; 1.
RM Transferase; DNA-directed RNA polymerase; Transcription.
RM SEQUENCE 264 AA; 29612 MW; C35B491B CRC32;
SQ
Query Match 30.7%; Score 62; DB 1; Length 264;
Best Local Similarity 47.4%; Pred. No. 6.40e-01;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Db 170 VTGNCERAVECPGEYF 188
Oy 2 vphlgdrektrdsvcpqgy 20
RESULT 9
ID SECA_TREPA STANDARD; PRT; 916 AA.
AC O83394;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.
DE SECA OR TP0379.
GN Treponema pallidum.
OS Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLES;
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SCHREGER E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HARCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RL spirochete".
RL Science 281:375-388(1998).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SECE
CC SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF
CC ATP TO THE TRANSFER OF PRE-SECRETORY PERIPLASMIC AND OUTER
CC MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
CC WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECH
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF PLASMA MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
CC -----
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AE001217; AAC65365.1;
RM TIGR: TP0379;
RM PFM: PF01043; SecA protein; 1.
RM Protein transport; ATP-binding; Membrane; Translocation; Transport.
RM NP_BIND 103 110 ATP (POTENTIAL).
RM SEQUENCE 916 AA; 103779 MW; 84D5AFAC CRC32;
SQ

```



```
CC the European Bioinformatics Institute. There are no restrictions on it
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb.sib.ch).
CC -----
DR EMBL; Z95620; CAB09117.1; -.
DR PFAM; PF01423; Sm; 1.
RW Hypothetical protein; Nuclear protein; Ribonucleoprotein.
SQ SEQUENCE 140 AA; 16171 MW; 4A092112C CRC32;
Query Match      29.2%; Score 59; DB 1; Length 140;
Best Local Similarity 31.8%; Pred. NO. 2.65e+00;
Matches       7; Conservative    8; Mismatches   7; Indels     0; Gaps    0;
DB      106 LAKHEERKKRNIREKGYLNS 127
OY      2 vphlgdrkrdsvcpqgkylnp 23
:: | : ||: :: ||| |:
RESULT 13
ID INT6_MOUSE STANDARD; PRT; 445 AA.
AC Q64252; Q64058; Q64059;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VIRAL INTEGRATION SITE PROTEIN INT-6.
DN INT6 OR INT-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NM [1]
RP SEQUENCE FROM N.A.
RA MARCHETTI A., BUTTITTA F., MIYAZAKI S., GALLAHAN D., SMITH G.H.,
RA CALLAHAN R.;
RT "Int-6, a highly conserved, widely expressed gene, is mutated by
RL mouse mammary tumor virus in mammary preneoplasia.";
RJ J. Virol. 69:1932-1938(1995).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE; 97405883.
RX DIELLA F., LEVI G., CALLAHAN R.;
RT "Characterization of the INT6 mammary tumor gene product.";
RL DNA Cell Biol. 16:839-847(1997).
[3]
RP REVISIONS TO N-TERMINUS.
RA CALLAHAN R.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS AT DAY 8 OF EMBRYONIC
CC DEVELOPMENT.
CC -1- DISEASE: INT-6 SERVES AS A SITE FOR VIRAL INTEGRATION OF MOUSE
CC MAMMARY TUMOR VIRUS (MMTV) IN MAMMARY TUMORS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC The European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb.sib.ch).
-----
DR EMBL; L35556; AB97930.1; -.
DR EMBL; S75221; AAC00046.1; -.
DR EMBL; S75223; AAC00047.1; -.
DR MGD; MG1:99257; INT6.
DR PFAM; PF01399; PCI; 1.
KW Proto-oncogene.
FT VARIANT 158 158 V -> N (IN MMTV-INDUCED TUMOR 1139-1).
FT VARIANT 159 445 MISSING (IN MMTV-INDUCED TUMOR 1139-1).
FT VARIANT 158 180 VPATRNALSTSLMGTLAEILLMQ -> LPQSDLEATGVTC
```

```

FT FT GTTAKVWMDK (IN MATV-INDUCED TUMOR  

FT VARIANT 318 365 LVANDFLVACLEDPIENARLFIFETFCRIHOCISIMLA  

FT VARIANT 318 365 DLKNMTE -> LKIKFQSSGIRYQAVSGMEIIRA  

FT VARIANT 318 365 AVGRPEGHRLRGDPLEENG (IN MATV-INDUCED  

FT SEQUENCE 445 AA; 52220 MW; E7ZIC93 CRC32;  

DB 66 IPH-ALREKRTVAOLKOLAETPEPT 91  

Oy 2 vphlgdrekrdsvcpqgkyhlpqxns1 28  

RESULT 14 Score 59; DB 1; Length 445;  

ID PSS1_HUMAN STANDARD; PRT; 473 AA.  

AC P48651;  

DT 01-FEB-1996 (Rel. 33, Created)  

DT 01-FEB-1996 (Rel. 33, Last sequence update)  

DT 01-NOV-1997 (Rel. 35, Last annotation update)  

DE PHOSPHATIDYL SERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-)  

DE (K1A0024).  

GN PSSA.  

OS Homo sapiens (Human).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  

OC Eutheria; Primates; Catarrhini; Homidae; Homo.  

RN [1]  

RP SEQUENCE FROM N.A.  

RC TISSUE=BONE MARROW;  

RX MEDLINE; 96051387.  

RA NOMURA N., MIYAJIMA N., SAZUKA T., TANAKA A., KAWABAYASHI Y.,  

RA SANO S., NAGASE T., SEKI N., ISHIKAWA K.-I., TABATA S.;  

RT "Prediction of the coding sequences of unidentified human genes. I.  

RT The coding sequences of 40 new genes (K1A0001-K1A0040) deduced by  

RT analysis of randomly sampled cDNA clones from human immature myeloid  

RT cell line KG-1.";  

RT DNA Res. 1:27-35(1994).  

CC - FUNCTION: BASE-EXCHANGE REACTION BETWEEN FREE L-SERINE AND THE  

CC POLAR HEAD GROUPS OF PRE-EXISTING PHOSPHOLIPIDS. IT CAN UTILIZE  

CC PHOSPHATIDYLCHOLINE AS A PHOSPHATIDYL DONOR. IT CAN ALSO CATALYZES  

CC THE CHOLINE AND ETHANOLAMINE BASE-EXCHANGE REACTIONS.  

CC - PATHWAY: COMMITTED STEP IN THE SYNTHESIS OF PHOSPHATIDYL SERINE.  

CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  

-----  

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  

CC the European Bioinformatics Institute. There are no restrictions on  

CC use by non-profit institutions as long as its content is in no way  

CC modified and this statement is not removed. Usage by and for commercial  

CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/  

CC or send an email to license@isb-sdb.ch).  

-----  

CC EMBL; D14694; BAA03520.1; -;  

KW Transferrase; Phospholipid biosynthesiss; Transmembrane.  

DR TRANSMEM 36 56 POTENTIAL.  

FT TRANSMEM 73 93 POTENTIAL.  

FT TRANSMEM 103 123 POTENTIAL.  

FT TRANSMEM 161 181 POTENTIAL.  

FT TRANSMEM 187 207 POTENTIAL.  

FT TRANSMEM 217 237 POTENTIAL.  

FT TRANSMEM 287 307 POTENTIAL.  

FT TRANSMEM 310 330 POTENTIAL.  

FT TRANSMEM 356 376 POTENTIAL.  

FT TRANSMEM 384 404 POTENTIAL.  

SQ SEQUENCE 473 AA; 55527 MW; D81JF6P2 CRC32;  

Query Match 29.2%; Score 59; DB 1; Length 473;  

Best Local Similarity 37.0%; Pred. No.2.65e+00;  

Matches 10; Conservative 10; Mismatches 6; Indels 1; Gaps 1;  


```

DB 408 HYGHEKTSCECDGT 424
 QY 4 hlgdrekdvcpqky 20

```

RESULT 15
ID 66PL CLAMI STANDARD; PRT; 568 AA.
AC P54237;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI) (EC 5.3.1.9)
DE (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHT).
GN PGIC1
OS Clarkia miltrediae;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosid II; Myrtales; Onagraceae; Clarkia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-POPULATION WEEDEN 165A;
RA GOTTLEIB L.D., FORD V.S.;
RT "Phylogenetic relationships among the sections of Clarkia (Onagraceae)
RT inferred from the nucleotide sequences of PgiC."
RL Syst. Bot. 21:1-18(1996)
CC -1- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE -> FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X89389; CAA61569.1; -.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
DR PRAM: PF00342; PGI; 1.
KW Glucneogenesis; Glycolysis; Isomerase; Multigene family.
SQ SEQUENCE 568 AA; 62664 MW; 703D6218 CRC32;

Query Match 29.2%; Score 59; DB 1; Length 568;
Best Local Similarity 41.7%; Pred. No. 2.65e+00;
Matches 10; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

DB 95 VLVHVALRPRDSAICSDGNVPPD 118
QY 2 vphlgdrekdv-vcpqkylnhpq 24
  
```

Search completed: Tue Apr 18 11:07:36 2000
 Job time : 31 secs.

 W P E R E H (TM)

Release 3.1A John F. Collins, BioComputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 18 11:07:54 2000; Maspar time 66.86 Seconds

Tabular output not generated.

Title: >PEP1.PEP
 Description: (1-28) from new pep
 Perfect Score: 202
 Sequence: 1 lvphlgdrekrdsvcpqgkylnhpqxnsl 28

Scoring table: PAM 150
 Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database:

sptrembl12
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 28.745; Variance 34.322; scale 0.837

*Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	167	82.7	189	6	TUMOUR NECROSIS FACTOR	4.85e-29
2	149	73.8	471	6	TUMOR NECROSIS FACTOR	1.26e-23
3	145	71.8	189	6	TUMOR NECROSIS FACTOR	1.93e-22
4	74	36.6	213	2	TUMOR NECROSIS FACTOR	2.98e-03
5	69	34.2	132	11	EMS/FLII ACTIVATED TRA	4.07e-02
6	68	33.7	483	3	OXIDOREDUCTASE	6.77e-02
7	66	32.7	467	5	PJCHI-3	1.85e-01
8	65	32.2	687	5	THROMBOSPONDIN RELATED	3.04e-01
9	65	32.2	1376	5	5 ALPHA FIBRILLAR COLL	3.04e-01
10	65	32.2	1724	5	P-GLYCOPROTEIN	3.04e-01
11	63	31.2	506	10	SQUALENE EPOXIDASE HOM	8.05e-01
12	63	31.2	518	10	SQUALENE EPOXIDASE HOM	8.05e-01
13	63	31.2	563	14	L PROTEIN	8.05e-01
14	62	30.7	307	10	F7H1.9 PROTEIN	1.30e+00
15	62	30.7	414	5	SQUALENE SYNTHASE	1.30e+00
16	62	30.7	563	2	ACTIVATOR	1.30e+00
17	62	30.7	699	1	699AA LONG HYPOHETICA	1.30e+00
18	62	30.7	774	3	POTATIVE ALPHA-NAYLISA	1.30e+00
19	62	30.7	1187	2	ENDOXANASE (EC 3.2.1	1.30e+00
20	62	30.7	2664	5	VARIANT-SPECIFIC SUPRA	1.30e+00

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
21	61	30.2	313	3	CONSERVED HYPOTHETICAL	2.09e+00
22	61	30.2	336	10	T30D6.19 PROTEIN	2.09e+00
23	61	30.2	563	2	PHR GENE	2.09e+00
24	61	30.2	837	4	KIAA0688 PROTEIN	2.09e+00
25	61	30.2	850	2	MAINOPEPTIDASE N	2.09e+00
26	61	30.2	3623	11	INTRINSIC FACTOR-B12 R	2.09e+00
27	60	29.7	88	2	RPSR2	3.34e+00
28	60	29.7	89	3	HYDROPHOBIN	3.34e+00
29	60	29.7	313	1	CONSERVED HYPOTHETICAL	3.34e+00
30	60	29.7	696	14	ORF K10	3.34e+00
31	60	29.7	696	14	ORF K10	3.34e+00
32	60	29.7	928	4	ORF K10	3.34e+00
33	60	29.7	3034	11	KIAA1008 PROTEIN	3.34e+00
34	60	29.7	3432	14	SEVEN-PASS TRANSMEMBR	3.34e+00
35	59	29.2	245	4	POLYPROTEIN PRECURSOR	3.34e+00
36	59	29.2	406	10	CARBOXY-PROPEPTIDE OF	5.30e+00
37	59	29.2	431	4	G-BOX BINDING PROTEIN	5.30e+00
38	59	29.2	445	4	HRHFE2060 PROTEIN (FR	5.30e+00
39	59	29.2	473	11	EUKARYOTIC TRANSLATION	5.30e+00
40	59	29.2	564	11	PHOSPHATIDYL SERINE SYN	5.30e+00
41	59	29.2	614	5	COLLAGEN ALPHA 1 (III)	5.30e+00
42	59	29.2	1544	4	REDA (FRAGMENT)	5.30e+00
43	59	29.2	1580	4	PLU-1 PROTEIN	5.30e+00
44	58	28.7	769	2	RETINOBLASTOMA BINDING	8.37e+00
45	58	28.7	3432	14	GLYCOSIDASE OLER	8.37e+00

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	167	82.7	189	6	TUMOUR NECROSIS FACTOR	4.85e-29
2	149	73.8	471	6	TUMOR NECROSIS FACTOR	1.26e-23
3	145	71.8	189	6	TUMOR NECROSIS FACTOR	1.93e-22
4	74	36.6	213	2	TUMOR NECROSIS FACTOR	2.98e-03
5	69	34.2	132	11	EMS/FLII ACTIVATED TRA	4.07e-02
6	68	33.7	483	3	OXIDOREDUCTASE	6.77e-02
7	66	32.7	467	5	PJCHI-3	1.85e-01
8	65	32.2	687	5	THROMBOSPONDIN RELATED	3.04e-01
9	65	32.2	1376	5	5 ALPHA FIBRILLAR COLL	3.04e-01
10	65	32.2	1724	5	P-GLYCOPROTEIN	3.04e-01
11	63	31.2	506	10	SQUALENE EPOXIDASE HOM	8.05e-01
12	63	31.2	518	10	SQUALENE EPOXIDASE HOM	8.05e-01
13	63	31.2	563	14	L PROTEIN	8.05e-01
14	62	30.7	307	10	F7H1.9 PROTEIN	1.30e+00
15	62	30.7	414	5	SQUALENE SYNTHASE	1.30e+00
16	62	30.7	563	2	ACTIVATOR	1.30e+00
17	62	30.7	699	1	699AA LONG HYPOHETICA	1.30e+00
18	62	30.7	774	3	POTATIVE ALPHA-NAYLISA	1.30e+00
19	62	30.7	1187	2	ENDOXANASE (EC 3.2.1	1.30e+00
20	62	30.7	2664	5	VARIANT-SPECIFIC SUPRA	1.30e+00

RP SEQUENCE FROM N.A.
 RC TISSUE-AORTA;
 RA LEE E.-K., TALYOR M.J., KEHRLI M.E.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U90937; AAB65143.1; -
 DR HSSP: P19438; 1TNR.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PFAM; PF00531; death; 1.
 DR PFAM; PF00020; TNFR_C6; 3.
 DR SEQUENCE 471 AA; 51367 MW; 1D60FPA4 CRC32;
 SO
 Query Match 73.8%; Score 149; DB 6; Length 471;
 Best Local Similarity 71.4%; Pred. No. 1.26e-23;
 Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 DB 30 LYPHGDLEKRESPOGKYNHPQNSTI 57
 1 LYPHGDLEKREKIDSVCPGKYIHQXNSI 28
 ID 097530 PRELIMINARY; PRT; 189 AA.
 AC 097530;
 DT 01-MAY-1999 (TREMblrel. 10; Created)
 DT 01-MAY-1999 (TREMblrel. 10; Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12; Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA DUTHIE S., NASIR I., ARGYLE D.J., ECKERSALL P.D.;
 RL "Canine tumor necrosis factor receptor, partial cds."
 DR EMBL; AF013955; AAD01516.1; -
 DR HSSP; P19438; 1TNR.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR Receptor.
 KW NON_TER
 FT NON_TER 189
 SO SEQUENCE 189 AA; 21324 MW; 2A93BEF CRC32;
 Query Match 71.8%; Score 145; DB 6; Length 189;
 Best Local Similarity 67.9%; Pred. No. 1.93e-22;
 Matches 19; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 DB 30 LYPHPRNRKRAILCPQGRYHPQDDSI 57
 1 LYPHGDLEKREKIDSVCPGKYIHQXNSI 28
 QY
 RESULT 4
 ID 032029 PRELIMINARY; PRT; 213 AA.
 AC 032029;
 DT 01-JAN-1998 (TREMblrel. 05; Created)
 DT 01-JAN-1998 (TREMblrel. 05; Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08; Last annotation update)
 DE YRR1 PROTEIN.
 GN Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA MEDLINE; 98044033.
 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENZOT F., DEVANE K.M., DOSTERHOF A., EHRLICH S.D., EMMERSON P.T.,

RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
 RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
 RA GRIM S.Y., GLASER P., GOFFEAU A., GOLIGITLY E.J., GRANDI G.,
 RA GUSEPPI G., GUY B.J., HAGA K., HAIBCH J., HARMOD C.R., HENAUT A.,
 RA HILBERT H., HOLAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
 RA JORIS B., KARAKATA D., KASHARA Y., KLAER-BLANCHARD M., KLEIN C.,
 RA KOBAYASHI Y., KOETTER P., KONIGSTEIN G., KROGH S., KUMANO M.,
 RA KURITA K., LAPIDUS A., LARDINOIS S., LABER J., LAZAREVIC V.,
 RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAHEL C., MEDIGUE C.,
 RA MEDINA N., MELIENDO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMARA A., ODEGA B., PARK S.H.,
 RA PARRO V., POHL T.M., PORTELELL D., PORROLIK S., PRESCOTT A.M.,
 RA PRESECAN E., PUJIC P., PURTELLE B., RAPPORT G., REY M., REYNOLDS S.,
 RA RIGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADATE Y.,
 RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFONE F.,
 RA SERIGUCHI J., SEKONKA A., SEROK S.J., SERROR F., SHIN B.S., SOLDI B.,
 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEKAWA K.,
 RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANIER F., VASSAROTI A.,
 RA VIARI A., MAMBUUT R., WEDLER E., WEDLER H., WEITZENEGGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUNO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZIMSTEIN E., YOSHIKAWA H., DANCHIN A.,
 RA "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis."
 RL Nature 390:249-256(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; 299117; CAB14670.1; -
 DR PFAM; PF00398; Rnadad; 1.
 DR SEQUENCE 213 AA; 24196 MW; ED4EFC11 CRC32;
 SO
 Query Match 36.6%; Score 74; DB 2; Length 213;
 Best Local Similarity 40.0%; Pred. No. 2.98e-03;
 Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 DB 119 HLTDEKRAIKQVKGKYLHDKIV 143
 4 HLTDEKREKIDSVCPGKYIHQXNSI 28
 QY
 RESULT 5
 ID 035324 PRELIMINARY; PRT; 132 AA.
 AC 035324;
 DT 01-JAN-1998 (TREMblrel. 05; Created)
 DT 01-JAN-1998 (TREMblrel. 05; Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 12; Last annotation update)
 DE EMS/FLII ACTIVATED TRANSCRIPT 2.
 GN EAT-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 97152556.
 RA THOMPSON A.D., BRAUN B.S., ARVAND A., STEWART S.D., MAY W.A., CHEN E.,
 RA KORENBERG J., DENNY C.;
 RA "EAT-2 is a novel SH2 domain containing protein that is up regulated
 RT by Ewing's sarcoma EMS/FLII fusion gene."
 RL Oncogene 13:2649-2658(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC THOMPSON A.D., BRAUN B.S., ARVAND A., STEWART S.D., MAY W.A., CHEN E.,
 RA KORENBERG J., DENNY C.;
 RA Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF020263; AAB70923.1; -
 DR HSSP; P12931; 1SHD.
 DR PFAM; PF00017; SH2; 1.
 DR SEQUENCE 132 AA; 15258 MW; 3126FD44 CRC32;
 SO
 Query Match 34.2%; Score 69; DB 11; Length 132;


```

RESULT 10
ID Q25425; PRELIMINARY; PRT; 1724 AA.
AC Q25425;
DE 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE P-GLYCOPROTEIN.
OS Leishmania tarentolae (Sauriella leishmania tarentolae).
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TARI;
RX MEDLINE; 95198776.
RA LEGARE D., HETTEMER E., OUELLETTE M.;
RT "The P-glycoprotein-related gene family in Leishmania.";
RL MCL Biochem. Parasitol. 68:81-91(1994).
DR EMBL; I29485; AAA5541.1; -.
DR HSSP; P13869; INED.
DR PFAM; PF00664; ABC_membrane; 2.
DR PFAM; PF00005; ABC_tran; 2.
SQ SEQUENCE 1724 AA; 188967 MW; C9F31C24 CRC32;

Query Match 32.28; Score 65; DB 5; Length 1724;
Best Local Similarity 40.0%; Pred. No. 3.04e-01;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 913 LDAHGERVMBRCIC 927
QY 1 LVPHGDKRDKSVC 15

RESULT 11
ID Q65727; PRELIMINARY; PRT; 506 AA.
AC Q65727;
DE 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SQUALENE EPOXIDASE HOMOLOGUE (EC 1.14.99.7) (SQUALENE MONOOXYGENASE).
GN SGP1.1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WESTAR; TISSUE-SHOOTS;
RA SCHAFER U.A., REED D.W., HUNTER D.G., YAO K., WENINGER A.M.,
RA TSANG E.W.T., REANEY M.J.T., MACKENZIE S.L., COVELLO P.S.;
RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
DE -1- CATALYTIC ACTIVITY: SQUALENE + AH(2) + O(2) - (S)-SQUALENE-2,3-
CC EPOXIDE + A + H(2)O.
CC -1- CORFACTOR: FAD.
CC EMBL; AJ005931; CA06773.1; -.
DR MENDEL; 29854; Brana;3399;29854.
KW Oxidoreductase.
SQ SEQUENCE 506 AA; 55571 MW; 04226965 CRC32;

Query Match 31.28; Score 63; DB 10; Length 506;
Best Local Similarity 30.0%; Pred. No. 8.05e-01;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

DB 74 HYTERDMREPVBMGEFMP 93
QY 4 HLGDKRDKSVCVPGKYLHP 23

RESULT 12
ID Q65726; PRELIMINARY; PRT; 518 AA.
AC Q65726;
DE 01-AUG-1998 (TREMBlrel. 07, Created)

```

```

DE 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SQUALENE EPOXIDASE HOMOLOGUE (EC 1.14.99.7).
GN SGP1.2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WESTAR; TISSUE-SHOOTS;
RA SCHAFER U.A., REED D.W., HUNTER D.G., YAO K., WENINGER A.M.,
RA TSANG E.W.T., REANEY M.J.T., MACKENZIE S.L., COVELLO P.S.;
RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ005928; CA06770.1; -.
DR MENDEL; 29850; Brana;3399;29850.
KW Oxidoreductase.
SQ SEQUENCE 518 AA; 57400 MW; 5F28687E CRC32;

Query Match 31.28; Score 63; DB 10; Length 518;
Best Local Similarity 30.0%; Pred. No. 8.05e-01;
Matches 6; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

DB 75 HYTERDMREPVBMGEFMP 94
QY 4 HLGDKRDKSVCVPGKYLHP 23

RESULT 13
ID Q82794; PRELIMINARY; PRT; 563 AA.
AC Q82794;
DE 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE L PROTEIN.
GN MBGGENE.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/PPV/DUTCH/27 (H7N7), DUTCH;
RA MUNK K., PRITZER E., KRETSCHMAR E., GUTTE B., GARTEN W., KLENK H.;
RL Glycobiology 0:0-0(1992).
DR EMBL; Z12617; CA078263.1; -.
DR PFAM; PF00509; Hemagglutinin; 1.
DR PRINTS; PR00329; HEMAGGLUTININ2.
DR PRINTS; PR00330; HEMAGGLUTININ1.
DR PRINTS; PR00331; HEMAGGLUTININ2.
SQ SEQUENCE 563 AA; 62883 MW; 6D36FAC1 CRC32;

Query Match 31.28; Score 63; DB 14; Length 563;
Best Local Similarity 33.38; Pred. No. 8.05e-01;
Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

DB 97 ERRERNDVCYGRFVNGE 114
QY 7 DREKIDSVCPGKYLHPQ 24

RESULT 14
ID Q9X111; PRELIMINARY; PRT; 307 AA.
AC Q9X111;
DE 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE F7H1.9 PROTEIN.
GN F7H1.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

```

OC Arabidopsis.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA LIN X., KAUT S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
 RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
 RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
 RA FRASER C.M., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence.";
 RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007134; AAD26930.1; -;
 SQ SEQUENCE 307 AA; 33640 MM; 079BE7E6 CRC32;

Query Match 30.7%; Score 62; DB 10; Length 307;
 Best Local Similarity 50.0%; Pred. No. 1.30e+00;
 Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

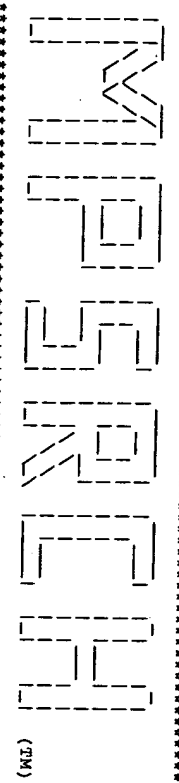
DB 253 LPHPRATGKRTPNOCPPGR 272
 QY 1 lvphlgdrekrdsv-cpqrk 19

RESULT 15
 ID 025308 PRELIMINARY; PRT; 414 AA.
 AC 025308;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE SQUALENE SYNTHASE.
 OS Leishmania major.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN VI;
 RA COFRIM P.C., GARITY L., BEVERLEY S.M.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U30455; AAC17923.1; -;
 DR PIRAM; PR00494; SOS_PSY.1.
 SQ SEQUENCE 414 AA; 46844 MM; FB8AA048 CRC32;

Query Match 30.7%; Score 62; DB 5; Length 414;
 Best Local Similarity 40.0%; Pred. No. 1.30e+00;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

DB 48 VVAQLADQQLDAIC 62
 QY 1 lvphlgdrekrdsvc 15

Search completed: Tue Apr 18 11:09:07 2000
 Job time : 73 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MSPch.p protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 18 11:05:10 2000; Maspar time 24.88 Seconds
Tabular output not generated. 26.654 Million cell updates/sec

Title: >PEP1.PEP
(1-28) from new.pep
Perfect Score: 202
Sequence: 1 lvpnlgtrekrdsvcpgkyihpqnsl 28

Scoring table: PAM 150
Gap 15

Searched: 188963 segs, 23686106 residues
Post-processing: Minimum Match 0%

Database: a-genebank
1:genebank

Statistics: Mean 21.488; Variance 63.322; scale 0.339

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	202	100.0	28	1	R1072	Peptide fragment #1 of	1.00e-16
2	202	100.0	102	1	R10984	Partial sequence 30kd	1.00e-16
3	202	100.0	154	1	R24082	Truncated TNF-alpha 55	1.00e-16
4	202	100.0	159	1	R24083	Truncated TNF-alpha 55	1.00e-16
5	202	100.0	158	1	R24084	Truncated TNF-alpha 55	1.00e-16
6	202	100.0	159	1	R24080	Truncated TNF-alpha 55	1.00e-16
7	202	100.0	211	1	W89225	Tumour necrosis factor	1.00e-16
8	202	100.0	309	1	W89228	Tumour necrosis factor	1.00e-16
9	202	100.0	311	1	W89228	Tumour necrosis factor	1.00e-16
10	202	100.0	366	1	W89228	Tumour necrosis factor	1.00e-16
11	202	100.0	371	1	W89228	Tumour necrosis factor	1.00e-16
12	202	100.0	397	1	W89227	Tumour necrosis factor	1.00e-16
13	202	100.0	417	1	W89226	Tumour necrosis factor	1.00e-16
14	202	100.0	420	1	W89226	Tumour necrosis factor	1.00e-16
15	202	100.0	433	1	R51032	Mutant p55 tumour necr	1.00e-16
16	202	100.0	443	1	R51033	Mutant p55 tumour necr	1.00e-16
17	202	100.0	451	1	R70107	TNF-R-GPB 130 fusion p	1.00e-16
18	202	100.0	455	1	R42059	Type I TNF receptor.	1.00e-16
19	202	100.0	455	1	R42059	Lambda derived TNF-R.	1.00e-16
20	202	100.0	455	1	R42197	p55 tumour necrosis fa	1.00e-16
21	202	100.0	455	1	R51034	Mutant p55 tumour necr	1.00e-16
22	202	100.0	455	1	R75084	p55 TNF-R.	1.00e-16
23	202	100.0	455	1	R07451	Human Tumour Necrosis	1.00e-16

24	202	100.0	455	1	R24000	TNF-alpha 55kd recepto	1.00e-16
25	202	100.0	455	1	R1082	Human 55kd TNF-binding	1.00e-16
26	202	100.0	455	1	R10986	30kd TNF inhibitor pre	1.00e-16
27	202	100.0	547	1	R70104	TNF-R-GPB fusion prot	1.00e-16
28	202	100.0	900	1	R70103	TNF-R-GPB 130 fusion p	1.00e-16
29	202	100.0	909	1	W64485	Human Fas protein.	1.00e-16
30	202	100.0	1245	1	R70106	TNF-R-PI. VIVAX DUFFY	1.00e-16
31	202	100.0	1604	1	R70105	TNF-R-PI. VIVAX DUFFY	1.00e-16
32	194	96.0	455	1	R20787	TNF-R-PI. VIVAX DUFFY	1.00e-16
33	190	94.1	884	1	R70109	TNF-alpha binding prot	1.00e-16
34	167	82.7	461	1	R07450	TNF-R-GPB 130 fusion p	1.00e-16
35	138	68.3	20	1	R41491	Rat Tumour Necrosis fa	4.00e-12
36	118	58.4	21	1	P91073	TNF inhibitory peptide	2.59e-08
37	118	58.4	106	1	W89235	N-terminal sequence of	8.78e-06
38	118	58.4	109	1	W89237	Protein SEQ ID NO:82 f	8.78e-06
39	118	58.4	110	1	W52274	Protein SEQ ID NO:84 f	8.78e-06
40	118	58.4	110	1	W52274	Truncated sTNF prot	8.78e-06
41	118	58.4	161	1	W52267	Soluble tumour necrosi	8.78e-06
42	118	58.4	161	1	R27496	Native 30 kd TNF inh	8.78e-06
43	118	58.4	161	1	W59664	Human soluble tumour n	8.78e-06
44	118	58.4	256	1	W33357	TBP(20-161)/hcg-alpha	8.78e-06
45	118	58.4	307	1	W33358	TBP(20-161)/hcg-beta	8.78e-06

ALIGNMENTS

RESULT 1	ID	R1072	standard; peptide; 28 AA.
AC	R1072;		
DE	24-MAY-1991 (first entry)		
DT	Peptide fragment #1 of 55kd TNF-binding protein.		
DR	Tumour Necrosis Factor; binding proteins; septic shock;		
KW	autoimmune glomerulonephritis; lymphokine; cytokine.		
KW	EP-417563-A.		
PD	20-MAR-1991.		
PF	31-AUG-1990; 116707.		
PR	12-SEP-1989; CH-003319.		
PR	08-MAR-1990; CH-000746.		
PR	20-APR-1990; CH-001347.		
PA	(HOFF) HOFFMANN-LA ROCHE AG.		
PI	Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;		
PI	Schlaeger EJ.		
DR	WPI, 91-081851/12.		
PT	Insoluble tumour necrosis factor binding proteins - and DNA		
PT	encoding them, useful in pharmaceutical prods. and for antibody		
PT	prodn.		
PS	Claim 3; Page 19; 26pp; German.		
CC	Cells which produce TNF-binding proteins (-BP) (eg HL60 cells) were		
CC	cultured and the supernatant centrifuged, put on a column of		
CC	"Affigel 10" to which recombinant TNF-alpha was bonded, and TNF-BP		
CC	eluted. The recovered protein was used as an immunogen to raise		
CC	monoclonal antibodies. The MAbs were attached to Sepharose 4B and		
CC	cell extract purified on a system of: BSA-Sepharose 4B; Ab-Sepharose-		
CC	4B and TNF alpha-Sepharose 4B. Active TNF-BP were eluted from the		
CC	last two columns and separated by gel electrophoresis to identify		
CC	bands of mol. wt. 875, 65, 55, 51, 38, 36 and 34kd. Partial amino		
CC	acid sequences were determined for the 75 and 55kd proteins,		
CC	including the fragment given here which is a minimum sequence for		
CC	TNF-binding.		
CC	See also R1073-R1081 and Q10955-6.		
CC	Sequence 28 AA;		
QY	Query Match	100.0%; Score 202; DB 1; Length 28;	
QY	Best Local Similarity 100.0%; Pred. No. 1.00e-16;		
QY	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	1 LYPHLDREKRDVCPGKYIHPOXNSI 28		
QY	1 lvpnlgtrekrdsvcpgkyihpqnsl 28		
RESULT 2	ID	R10984	standard; protein; 102 AA.


```
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
SQ Sequence      154 AA;  
  
Query Match          100.0%; Score 202; DB 1; Length 154:  
Best Local Similarity   96.4% ; Pred. No. 1,00e-16;  
Matches     27; Conservative    0; Mismatches    1; Indels    0; Gaps    0;
```

```
Dd       30 LVPHLGDRERKRDVCPQGGKYIHPQNNSI 57  
         |||||  
Oy       1 LVPHLGIREKRIDSVCPQGKIYLPNPNMSL 28
```

```
RESULT           4  
ID R24083 standard; Protein; 159 AA.  
AC R24083:  
DT 05-NOV-1992 (first entry)  
DE Truncated TNF-alpha 55kD receptor.  
KW tumour necrosis factor alpha; extracellular binding domain; AIDS;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
SN W09207076-A.  
PD 30-APR-1992.  
PF 18-OCT-1991; G01826.  
PR 18-OCT-1990; GB-022648.  
PT (CHAR-) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FW, Feldmann M, Gray PW, Turner MJC,  
DR N-PSTD; Q24444.  
SR New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.
```

```
Pt Example 1; Fig 10; 43pp: English.  
Cc This sequence is a truncated TNF-alpha receptor derivative as encoded in peltatitl. This was produced as described in Q24444. This derivative lacks the third cysteine rich subdomain and sequestering human TNF-alpha e.g. in the treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, CC graft versus host disease and autoimmune diseases, esp. rheumatoid CC arthritis.  
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8 SQ Sequence      159 AA;
```

```
Sq Query Match          100.0%; Score 202; DB 1; Length 159:  
Best Local Similarity   96.4% ; Pred. No. 1,00e-16;  
Matches     27; Conservative    0; Mismatches    1; Indels    0; Gaps    0;
```

```
Dd       30 LVPHLGDRERKRDVCPQGGKYIHPQNNSI 57  
         |||||  
Oy       1 LVPHLGIREKRIDSVCPQGKIYLPNPNMSL 28
```

```
RESULT           5  
ID R24084 standard; Protein; 168 AA.  
AC R24084:  
DT 05-NOV-1992 (first entry)  
DE Truncated TNF-alpha 55kD receptor.  
KW tumour necrosis factor alpha; extracellular binding domain; AIDS;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
SN W09207076-A.  
PD 30-APR-1992.  
PF 18-OCT-1991; G01826.  
PR 18-OCT-1990; GB-022648.  
PT (CHAR-) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FW, Feldmann M, Gray PW, Turner MJC,  
DR N-PSTD; Q24445.  
SR New polypeptide capable of binding human TNF alpha - comprises
```

PT first three cysteine-rich subdomains of TNF alpha receptor for
 PS treating autoimmune disease, septic shock, HIV etc.
 CC Example 1; Fig 11; 43pp; English.
 CC This sequence is a truncated TNF-alpha receptor derivative, as
 CC encoded in pdeltarv. This was produced as described in Q24445.
 CC This derivative lacks the membrane proximal 4th subdomain, yet
 CC retains the ability to bind TNF-alpha with high affinity
 CC (10power8 - 10power9 Mpower-1). The deriv. can be used in the
 CC regulation of TNF-alpha mediated responses by binding and
 CC sequestering human TNF-alpha e.g. in the treatment of pulmonary
 CC diseases, septic shock, HIV infection, malaria, viral meningitis,
 CC graft versus host disease and autoimmune diseases, esp. Rheumatoid
 CC arthritis. The deriv. is given at 10-100ug/dose.
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
 SQ Sequence 168 AA;

Query Match 100.0%; Score 202; DB 1; Length 168;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDRERKDSVCPGKTYHPQNSI 57
 1 LVPHLGDRERKDSVCPGKTYHPQNSI 28

RESULT 6
 ID R24080 standard; Protein; 199 AA.
 AC R24080;
 DT 05-NOV-1992 (first entry)
 DE Truncated TNF-alpha 55kd receptor.
 KW Tumour necrosis factor alpha; extracellular binding domain;
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
 KW malaria; viral meningitis; graft versus host disease;
 KW autoimmune disease; rheumatoid arthritis.
 OS Homo sapiens.
 PN W09207076-A.
 PD 30-APR-1992.
 PF 18-OCT-1991; G01826.
 PR 18-OCT-1990; GB-022648.
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
 PI Brennan FM, Feldmann M, Gray FM, Turner MJC;
 DR WPI; 92-167156/20.
 DR N-PSDB; Q24441.
 PT New polypeptide capable of binding human TNF alpha - comprises
 PT first three cysteine-rich subdomains of TNF alpha receptor for
 PT treating autoimmune disease, septic shock, HIV etc.
 PS Example; Fig 7; 43pp; English.
 CC This sequence is a truncated TNF-alpha receptor derivative, as encoded
 CC in pTNFrecd. This was produced as described in Q24440.
 CC This derivative lacks the 81 carboxyl terminal residues of the
 CC cytoplasmic domain. The derivative could be used in the
 CC regulation of TNF-alpha mediated responses by binding and
 CC sequestering human TNF-alpha e.g. in the treatment of pulmonary
 CC diseases, septic shock, HIV infection, malaria, viral meningitis,
 CC graft versus host disease and autoimmune diseases, esp. Rheumatoid
 CC arthritis.
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
 SQ Sequence 199 AA;

Query Match 100.0%; Score 202; DB 1; Length 199;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDRERKDSVCPGKTYHPQNSI 57
 1 LVPHLGDRERKDSVCPGKTYHPQNSI 28

RESULT 7
 ID W89225 standard; Protein; 211 AA.
 AC W89225;
 DT 04-MAR-1999 (first entry)
 DE Tumour necrosis factor Dp/osteoprotegerin construct TNFBp 4.0.

KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OP; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN W09849305-A1.
 PD 05-NOV-1998;
 PF 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 DR WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OP) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OP and TNF receptor (TNFR)/OP chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFBp/OP construct from
 CC the example of the present invention for creating TNFBp/OP fusion
 CC proteins.
 SQ Sequence 211 AA;

Query Match 100.0%; Score 202; DB 1; Length 211;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLGDRERKDSVCPGKTYHPQNSI 57
 1 LVPHLGDRERKDSVCPGKTYHPQNSI 28

RESULT 8
 ID R70108 standard; Protein; 309 AA.
 AC R70108;
 DT 10-NOV-1995 (first entry)
 DE TNF-R-GBPH fusion protein.
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;
 KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A;
 KW tumour necrosis factor receptor; TNF-R.
 OS Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 FH Key Location/Qualifiers
 FT misc_difference 230..269
 FT /label="repeat_region
 FT /note="can be repeated n times, where n is a real
 FT number"
 PN W09506737-A.
 PD 09-MAR-1995.
 PF 01-SEP-1994; G01900.
 PR 03-SEP-1993; GB-018350.
 PR 23-AUG-1994; GB-017021.
 PA (PREN/) PRENDERGAST K F.
 PI Prendergast KF;
 DR WPI; 95-115452/15.
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.
 PS Example A; Page 54-55; 93pp; English.
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite

CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70103-23 are examples
CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor
CC receptor (in accordance with R Loetscher et al Cell, Vol. 61, 351-359)
CC and glycoprotein binding protein (GBP) homologue (GBPH). The
CC use of cytokine receptors not normally found on RBCs means that the
CC cytokine can bind harmlessly to the RBC without deleterious effect.
CC The RBC protects the hybrid peptides from excretion from the kidney, and
CC due to steric hindrance prevents the cytokines binding to a receptor in
CC another cell. GBP 130 or GBPH are the pref. malaria parasite peptides
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA
CC (pre major merozoite surface antigen) and the Duffy binding receptor
CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to
CC pref. glycoprotein A, B and C, sialo glycoproteins, found on the surface
CC of RBCs. The hybrid peptides are thus used to lower the levels of free
CC cytokines in the circulation to reduce pathological damage.

SO Sequence 309 AA;

Query Match

Best Local Similarity 96.4%; Pred. No. 1,00e-16;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 9 LYPHLDREKRDSCVCPGKYIHPPQNSI 36
QY 1 LYPHLDREKRDSCVCPGKYIHPPQNSI 28

RESULT 9

ID W89229 standard; Protein: 311 AA.

AC W89229;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.

KM Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

KM Inflammation; apoptosis.

OS Homo sapiens.

SN Synthetic.

PN MO9849305-A1.

PD 05-NOV-1998.

PF 29-APR-1998; U08631.

PR 01-MAY-1997; US-850188.

PA (AMGE-) AMGEN INC.

PI Boyle WJ, Wooden S;

DR WPI; 99-034661/03.

PT New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,

PT useful to treat TNF and TNFR-mediated disorders

PS Example 1; Fig 4; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising

CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous

CC amino acid sequence. Also described are: (1) a multimer polypeptide

CC comprising covalently associated A1 monomers; (2) an isolated nucleic

CC acid encoding A1; (3) an expression vector comprising the nucleic acid

CC sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products

CC from the present invention are useful to treat a variety of disorders

CC including those related to receptor binding. Compositions comprising

CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras

CC are used to treat TNF and TNFR-mediated disorders such as inflammation,

CC autoimmune diseases and disorders related to excessive apoptosis. The

CC chimeras are also useful for detecting molecules which interact with

CC fused heterologous sequences to identify potential new receptors and

CC ligands. The present sequence represents a TNFbp/OPG construct from

CC the example of the present invention for creating TNFbp/OPG fusion

CC proteins.

SO Sequence 311 AA;

Query Match

Best Local Similarity 100.0%; Score 202; DB 1; Length 311;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LYPHLDREKRDSCVCPGKYIHPPQNSI 57

QY 1 LYPHLDREKRDSCVCPGKYIHPPQNSI 28

RESULT 10

ID W89228 standard; Protein: 366 AA.

AC W89228;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.

KM Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

KM Inflammation; apoptosis.

OS Homo sapiens.

SN Synthetic.

PN MO9849305-A1.

PD 05-NOV-1998.

PF 29-APR-1998; U08631.

PR 01-MAY-1997; US-850188.

PA (AMGE-) AMGEN INC.

PI Boyle WJ, Wooden S;

DR WPI; 99-034661/03.

PT New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,

PT useful to treat TNF and TNFR-mediated disorders

PS Example 1; Fig 4; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising

CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous

CC amino acid sequence. Also described are: (1) a multimer polypeptide

CC comprising covalently associated A1 monomers; (2) an isolated nucleic

CC acid encoding A1; (3) an expression vector comprising the nucleic acid

CC sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products

CC from the present invention are useful to treat a variety of disorders

CC including those related to receptor binding. Compositions comprising

CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras

CC are used to treat TNF and TNFR-mediated disorders such as inflammation,

CC autoimmune diseases and disorders related to excessive apoptosis. The

CC chimeras are also useful for detecting molecules which interact with

CC fused heterologous sequences to identify potential new receptors and

CC ligands. The present sequence represents a TNFbp/OPG construct from

CC the example of the present invention for creating TNFbp/OPG fusion

CC proteins.

SO Sequence 366 AA;

Query Match

Best Local Similarity 100.0%; Score 202; DB 1; Length 366;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LYPHLDREKRDSCVCPGKYIHPPQNSI 57

QY 1 LYPHLDREKRDSCVCPGKYIHPPQNSI 28

RESULT 11

ID R07449 standard; Protein: 371 AA.

AC R07449;

DT 29-JUN-1991 (first entry)

DE Tumour Necrosis Factor-Binding Protein from PTFN-BP15 CDNA.

KM Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

KW PTFN-BP15; infectious disease; parasitic disease; cachexia;

KM autoimmune disease; shock.

OS Homo sapiens.

PN EP-393438-A.

PD 24-OCT-1990.

PF 06-APR-1990; 106624.

PR 21-APR-1989; DE-913101.

PR 21-JUN-1989; DE-920282.

PA (BOEH) BOEHRINGER INGELHEIMINT.

PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;

DR N-PSDB; Q06282.

PT DNA encoding TNF binding protein and TNF-receptor - used in

PT tumour treatment and to understand mechanism to TNF action

PT disclosure; Fig 1(1-3); 51pp; German.

CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of
 CC e.g. COS7 cells. The expressed proteins are useful
 CC prophylactically and therapeutically to control disorders which
 CC involve the damaging effects of TNF- α or beta (e.g. infectious or
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
 CC respiratory distress syndrome etc.), or side effects of treatment with
 CC TNF- α (alpha). They can also be used as diagnostic reagents for
 CC assaying TNF and in study of TNF-receptor interactions.
 CC See also 006282-006285.
 SQ Sequence 371 AA;

Query Match 100.0%; Score 202; DB 1; Length 371;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLDREKRDSCVCPGKRYHPONNSI 57
 |||||
 OY 1 LVPHLDREKRDSCVCPGKRYHPQXNSI 28

RESULT 12
 ID W89227 standard; Protein; 397 AA.
 AC W89227;
 DT 04-MAR-1999 (first entry)
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW Inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998.
 PE 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 DR WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 SQ Sequence 397 AA;

Query Match 100.0%; Score 202; DB 1; Length 397;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLDREKRDSCVCPGKRYHPONNSI 57
 |||||
 OY 1 LVPHLDREKRDSCVCPGKRYHPQXNSI 28

RESULT 13
 ID W89226 standard; Protein; 417 AA.
 AC W89226;
 DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/196.
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW Inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998.
 PE 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 DR WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFbp/OPG construct from
 CC the example of the present invention for creating TNFbp/OPG fusion
 CC proteins.
 SQ Sequence 417 AA;

Query Match 100.0%; Score 202; DB 1; Length 417;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 30 LVPHLDREKRDSCVCPGKRYHPONNSI 57
 |||||
 OY 1 LVPHLDREKRDSCVCPGKRYHPQXNSI 28

RESULT 14
 ID W89224 standard; Protein; 420 AA.
 AC W89224;
 DT 04-MAR-1999 (first entry)
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW Inflammation; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN MO9849305-A1.
 PD 05-NOV-1998.
 PE 29-APR-1998; U08631.
 PR 01-MAY-1997; US-850188.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Wooden S;
 DR WPI; 99-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR-mediated disorders
 PS Example 1; Fig 4; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products

CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumor necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents a TNFp/OPG construct from
 CC the example of the present invention for creating TNFp/OPG fusion
 CC proteins.
 CC Sequence 420 AA;

Query Match 100.0%; Score 202; DB 1; Length 420;
 Best Local Similarity 96.4%; Pred. No. 1.00e-16;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 30 LVPHLGDRKRDVCPQGIHPONNSI 57
 1 lvpplgdrkrdsvcpqgkylhpqxnsl 28

RESULT 15
 ID R51032 standard; Protein; 433 AA.
 AC R51032;
 DT 13-MAY-1994 (first entry)
 DE Mutant p55 tumour necrosis factor receptor.
 KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
 KW effector protein.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT region 1..21
 FT domain /label= leader peptide.
 FT 183..205 /label= transmembrane domain.
 PN EP-568925-A.
 PD 10-NOV-1993.
 PE 29-APR-1993; 106981.
 PR 03-MAY-1992; IL-101769.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Brakelusch C, Wallach D;
 DR N-PSDB: 050870.
 PT Modulating activity of tumour necrosis factor receptor - using
 PT peptide(s), antibodies, etc. which interact with critical regions
 PT of receptor or effector protein, for controlling auto-immune
 PT disease, septic shock, etc.
 PS Claim 4; Figure 1; 17pp; English.
 CC Modification of the tumour necrosis factor receptor by mutation or
 CC deletion modulates signal transduction and/or cleavage effected by
 CC the receptor. This modulation of activity can also be achieved
 CC using effector proteins which interact with the TNF receptor.
 CC Molecules which interact with the TNF receptor or the effector
 CC proteins can be used to treat or prevent diseases associated with
 CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
 CC rejection; graft vs. host disease or septic shock. They can also
 CC be used to treat overdoses of exogenous TNF. Specific deletions
 CC include amino acid residues 405-426 (to give this sequence, wild
 CC type protein disclosed in R42197) from which it was discovered
 CC that amino acids 405-414, or part of them, are essential for the
 CC signalling of the human p55 TNF-R for the cytotoxic effect of TNF
 CC whereas amino acids 415-426 are not essential. Also residues
 CC 170-174, 174-179 or both 1-170-179 were deleted. This region of
 CC amino acids, or part of, when deleted, abolished shedding of the
 CC soluble extracellular forms of the protein.
 SQ Sequence 433 AA;

Query Match 100.0%; Score 202; DB 1; Length 433;

Best Local Similarity 96.4%; Pred. No. 1.00e-16;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 30 LVPHLGDRKRDVCPQGIHPONNSI 57
 1 lvpplgdrkrdsvcpqgkylhpqxnsl 28

QY 1 lvpplgdrkrdsvcpqgkylhpqxnsl 28
 Search completed: Tue Apr 18 11:05:38 2000
 Job time : 28 secs.